

1 MetTyrlleTyrlleValAlaLeuValGlyPheLeuLeuAlaasnPro 20
6995 ATGATATTTACCTACCTTTTTCCTTTGCTTTAGCTTGCGGCTTTTACTTCTTAATCAAAATCCA
21 llaasnAlaaspLeuArgGlylleValGlySerProPheLeuAlaSerGlylleSerAsn 40
6935 ATCAATCGCGATTTACGAAAAATTGTTGGCTCACCATTTTACGCTCTCGAATTTCCAAC
41 pheValGlySerllePheLeuGlyllelleThrLeuValThrSerGlnThrLeuPhePro 60
6875 TTGTTGCTTCGATTTTTCAGCAATCATCATTACTGACCAAGTCAAAACATTTTCTCT
61 SerPheGlnPheValGlySerHisProValTrpIleTrpIleGlyValLeuGlyGly 80
6815 ACTTTTCAATTTGTTGCTTCACACCCACCATGCAATGCAATGCTGCTTCTTGGTGGG 6756
81 llePheLeuThrSerAsnValLeuPheProArgLeuGlyAlaValGlnThrVallle 100
6755 ATTTTCTAACGCTCATAGTTTACTTTTTCAGCATTAAGAGCTGTCTCAAAACAGTAT
101 LeuProilleLeuGlyArgilleLeuMetGlyThrLeuilleAspSerPheGlyTrpPheHis 120
6695 TTACCTATTTTGGCGTCAAAATATGATGGCGACACTTATTCATTTGGCTGGTTTCAT
121 AlaMetGlnLeuProMetThrLeuMetArgPheLeuGlyValillelleThrLeuAlaGly 140
6635 GCCATCGAACTTCGATCTGATCGGCTTTTTCGCAATTAATCATTTACTTACCTGCT 6576
141 ValilleValAlaValLeuProAsnLeuGlyGlySerGlnAlaGlnThrHisGlnThr 160
6575 GTTATTCGCTGGCGTTGTTCTTCCTAATTTAAACAAAAACAACGACCAACCAACT 6516
161 AsnLeuLeuGlyTrpArgilleTrpAlaValilleValGlyAlaMetSerAlaAlaGlnGln 180
6515 AACTTACTAGCGTCCGCGATATGCGCGGCTCATCGTTGCCCAATGTCAGCTGCTCAACA 6456
181 AlaIleAsnGlyArgLeuGlyValLeuLeuGlnAsnThrAlaGlnAlaThrPheValSer 200
6455 CCAATTAATGCGCCGATTCGCGAGTTTACTTGAAATACTGCAACAACGACGCTTTGTTCC 6396
201 PhePheilleGlyPheLeuAlaIlePheilleValSerLeuPheilleAspArgLeuPro 220
6395 TTCTTCATTCGATTTTACGCTATTTTTCGTTCTCTCTTTTATTCAGCACGCTTTGCCA 6336
221 LysilleSerGlnLeuLysLysAlaLysProTrpAsnGlyilleGlyGlyPheLeuGlyAla 240
6335 AAAATTCAGCAATTAACAAAAAGCAAAACCTTGCAATGCAATTCGCTGCATTTTACGAGCT 6276
241 SerilleValPheAlaThrValAlaValProGlnilleGlyAlaGlyLeuThrIleMet 260
6275 TCATTTGTTTTTCGAACAGTCTGTTGCTGTTCCGCAAAATTCGTCAGGCTCACAATATATC 6216
261 MetGlyLeuIleGlyGlnilleLeuGlySerMetLeuValGlnGlnPheGlyTrpTrpArg 280
6215 ATGGCTTCATTCGACAAAAATTTAGCGCAGTATGTTGCTTCACAACAAATTTGCTTGGCGC 6156
281 SerSerLysTrpGlyIleGlnIleTrpGlnIleValGlyIleLeuIleMetLeuThrGly 300
6155 TCAAGTAAATATGCGCATTCAAATTTGCAAAATTCGTCGATTCCTAATATATCTGACCGCA 6096
301 llellePheIleLysPheLeu 307
6095 ATAAATTCATTAATTTTAA 6075

RESULT 2

AB55104
ID AB55104 standard; protein; 307 AA.

AC AB55104;

DT 29-AUG-2002 (revised)

DT 16-MAY-2002 (first entry)

DE Lactococcus lactis protein y5b.

KB Biogenesis; biodegradation; lactic bacterium; yogurt; cheese.

OS Lactococcus lactis; IL1403.

PN FR007448-AL.

PD 12-OCT-2001.

PF 11-APR-2000; 2000FR-00004630.

PR 11-APR-2000; 2000FR-00004630.

RA (INRA) INRA INST NAT RECH AGRONOMIQUE.

PI Bolotine A, Sorokine A, Henault P, Ehrlich SD.

DB MPI; 2002-043410/06.

PT New nucleotide sequence useful in the identification of Lactococcus

PS lactis and related species.

XX Claim 6; SEQ ID NO 1006; 2504pp; French.

CC The present invention is related to a Lactococcus lactis nucleotide

CC sequence (AB550521) and related proteins (AB552300-AB555621). The nucleic

CC acid sequence is useful in the detection and/or amplification of nucleic

CC acid sequence, particularly to identify Lactococcus lactis or related

CC species. The proteins of the invention are useful for the biotechnologies or

CC biodegradation of a composition of interest. The invention helps research

CC in lactic bacteria, particularly useful in the production of yogurt and

CC cheese. Note: The sequence data for this patent is based on equivalent

CC patent WO200177334 (published 10-OCT-2001) which is available in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/publ/published_ptc_sequences. (Updated on 29-AUG-2002) to

CC standardize OS field)

XX Sequence 307 AA;

Query Match
Best Local Similarity 98.04; Pred. No. 9,4e-161;
98.54; Score 1529; DB 5; Length 307;
Matches 301; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MYIALATVCCFTLANQMPIMKIMLVCSPTLASGIZMWVCSISFLGIIITLVTSQTLFP 60

DB 1 MYIALATVCCFTLANQMPIMKIMLVCSPTLASGIZMWVCSISFLGIIITLVTSQTLFP 60

QY 61 SFQVCSHPSWQIWCGLGCTFLTSWVLTFFPLCAVGVLPILGRIIMNCTLIDISGLTH 120

DB 61 SFQVCSHPSWQIWCGLGCTFLTSWVLTFFPLCAVGVLPILGRIIMNCTLIDISGLTH 120

QY 121 AMQPMTHRLGCVIITLACVAVAPMLPKMKKCAETHTQWLTGARIWAVIVGAM3AAQ 180

DB 121 AMQPMTHRLGCVIITLACVAVAPMLPKMKKCAETHTQWLTGARIWAVIVGAM3AAQ 180

QY 101 AINCHLGVLTENLTAQATLVSTFTLFAITLVSTFTTHRLPKI3ELXKAKPQWNGICGLCA 240

DB 101 AINCHLGVLTENLTAQATLVSTFTLFAITLVSTFTTHRLPKI3ELXKAKPQWNGICGLCA 240

QY 141 SIIVATVAAPQICACLTITMAGLTCGMLVQGCWMB33KXGCIQWQIVGILMLTC 300

DB 141 SIIVATVAAPQICACLTITMAGLTCGMLVQGCWMB33KXGCIQWQIVGILMLTC 300

QY 301 IIFIKLT 307

DB 301 IIFIKLT 307